RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/568,488_

Source: _IFWP_

Date Processed by STIC: _2/23/06_

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 02/23/2006
PATENT APPLICATION: US/10/568,488   TIME: 07:58:36

        Input Set : A:\ISPH0859USASEQ.txt
        Output Set: N:\CRF4\02232006\J568488.raw

     4 <110> APPLICANT: Monia, Brett P.
     5   Dobie, Kenneth W.
     6   Freier, Susan M.
     7   Popoff, Ian
     8   Wong, Wai Shiu Fred
     9   Karras, James G.
    11 <120> TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
    12   Activated Protein Kinase Expression
    14 <130> FILE REFERENCE: ISPH-0859USA
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/568,488
C--> 17 <141> CURRENT FILING DATE: 2006-02-14
    17 <150> PRIOR APPLICATION NUMBER: PCT/US2004/026344
    18 <151> PRIOR FILING DATE: 2004-08-12
    20 <150> PRIOR APPLICATION NUMBER: US 10/641,455
    21 <151> PRIOR FILING DATE: 2003-08-15
    25 <160> NUMBER OF SEQ ID NOS: 412
    27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    29 <210> SEQ ID NO: 1
    30 <211> LENGTH: 1539
    31 <212> TYPE: DNA
    32 <213> ORGANISM: Homo sapiens
    34 <220> FEATURE:
    35 <221> NAME/KEY: CDS
    36 <222> LOCATION: (295)..(1377)
    38 <300> PUBLICATION INFORMATION:
    39 <303> JOURNAL: Science
    40 <304> VOLUME: 265
    41 <305> ISSUE: 5173
    42 <306> PAGES: 808-811
    43 <307> DATE: 1994-08-05
    44 <308> DATABASE ACCESSION NO: L35253
    45 <309> DATABASE ENTRY DATE: 1995-08-14
    47 <400> SEQUENCE: 1
    48 ggaattccgg gcccggtctt tcctcccgcc gccgccggcc tggtcccggg gactggcctc   60
    49 cacgtccgac tcgtccgagc tgaagcccag cagcactttg ctgccagccg cggggggcggc   120
    50 ggaggcgccc ccgggcccctc ccaggaggct ctctgggcca gaggccgaga ttcggcacag   180
    51 gcccccagga gtccgtaagt aggagaggtc gcccgagacc ggccggaccc ccatccccgc   240
    52 ggccgccgcc gccgctggtc ccgcggctgc gaccgtggcg gctgccgctg gaaa atg   297
    53   Met
    54   1
    56 tct cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag aca atc   345
    57 Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr Ile
    58   5   10   15

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```
 60 tgg gag gtg ccc gag cgt tac cag aac ctg tct cca gtg ggc tct ggc     393
 61 Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly
 62         20                  25                  30
 64 gcc tat ggc tct gtg tgt gct gct ttt gac aca aaa acg ggg tta cgt     441
 65 Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu Arg
 66         35                  40                  45
 68 gtg gca gtg aag aag ctc tcc aga cca ttt cag tcc atc att cat gcg     489
 69 Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His Ala
 70  50                  55                  60                  65
 72 aaa aga acc tac aga gaa ctg cgg tta ctt aaa cat atg aaa cat gaa     537
 73 Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His Glu
 74                  70                  75                  80
 76 aat gtg att ggt ctg ttg gac gtt ttt aca cct gca agg tct ctg gag     585
 77 Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu Glu
 78             85                  90                  95
 80 gaa ttc aat gat gtg tat ctg gtg acc cat ctc atg ggg gca gat ctg     633
 81 Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp Leu
 82         100                 105                 110
 84 aac aac att gtg aaa tgt cag aag ctt aca gat gac cat gtt cag ttc     681
 85 Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln Phe
 86         115                 120                 125
 88 ctt atc tac caa att ctc cga ggt cta aag tat ata cat tca gct gac     729
 89 Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asp
 90 130                 135                 140                 145
 92 ata att cac agg gac cta aaa cct agt aat cta gct gtg aat gaa gac     777
 93 Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu Asp
 94                 150                 155                 160
 96 tgt gag ctg aag att ctg gat ttt gga ctg gct cgg cac aca gat gat     825
 97 Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp Asp
 98             165                 170                 175
100 gaa atg aca ggc tac gtg gcc act agg tgg tac agg gct cct gag atc     873
101 Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile
102         180                 185                 190
104 atg ctg aac tgg atg cat tac aac cag aca gtt gat att tgg tca gtg     921
105 Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser Val
106         195                 200                 205
108 gga tgc ata atg gcc gag ctg ttg act gga aga aca ttg ttt cct ggt     969
109 Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly
110 210                 215                 220                 225
112 aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga acc    1017
113 Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly Thr
114                 230                 235                 240
116 cca ggg gct gag ctt ttg aag aaa atc tcc tca gag tct gca aga aac    1065
117 Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg Asn
118         245                 250                 255
120 tat att cag tct ttg act cag atg ccg aag atg aac ttt gcg aat gta    1113
121 Tyr Ile Gln Ser Leu Thr Gln Met Pro Lys Met Asn Phe Ala Asn Val
122         260                 265                 270
124 ttt att ggt gcc aat ccc ctg gct gtc gac ttg ctg gag aag atg ctt    1161
```

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```
125 Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met Leu
126        275              280              285
128 gta ttg gac tca gat aag aga att aca gcg gcc caa gcc ctt gca cat     1209
129 Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala His
130 290              295              300              305
132 gcc tac ttt gct cag tac cac gat cct gat gat gaa cca gtg gcc gat     1257
133 Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala Asp
134             310              315              320
136 cct tat gat cag tcc ttt gaa agc agg gac ctc ctt ata gat gag tgg     1305
137 Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu Trp
138             325              330              335
140 aaa agc ctg acc tat gat gaa gtc atc agc ttt gtg cca cca ccc ctt     1353
141 Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro Leu
142        340              345              350
144 gac caa gaa gag atg gag tcc tga gcacctggtt tctgttctgt tgatcccact    1407
145 Asp Gln Glu Glu Met Glu Ser
146        355              360
148 tcactgtgag gggaaggcct tttcacggga actctccaaa tattattcaa gtgcctcttg   1467
149 ttgcagagat ttcctccatg gtggaagggg gtgtgcgtgc gtgtgcgtgc gtgttagtgt   1527
150 gtgtgcatgt gt                                                       1539
153 <210> SEQ ID NO: 2
155 <400> SEQUENCE: 2
W--> 156 000
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 20
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: antisense sequence
167 <400> SEQUENCE: 3
168 aagaccgggc ccggaattcc                                                20
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 30
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: antisense sequence
178 <400> SEQUENCE: 4
179 gtggaggcca gtccccggga ccggaattcc                                     30
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: antisense sequence
190 <400> SEQUENCE: 5
191 tggcagcaaa gtgctgctgg                                                20
194 <210> SEQ ID NO: 6
195 <211> LENGTH: 20
```

```
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: antisense sequence
202 <400> SEQUENCE: 6
203 cagagagcct cctgggaggg                                         20
206 <210> SEQ ID NO: 7
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: antisense sequence
214 <400> SEQUENCE: 7
215 tgtgccgaat ctcggcctct                                         20
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 20
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: antisense sequence
226 <400> SEQUENCE: 8
227 ggtctcgggc gacctctcct                                         20
229 <210> SEQ ID NO: 9
230 <211> LENGTH: 20
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: antisense sequence
237 <400> SEQUENCE: 9
238 cagccgcggg accagcggcg                                         20
241 <210> SEQ ID NO: 10
242 <211> LENGTH: 20
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: antisense sequence
249 <400> SEQUENCE: 10
250 cattttccag cggcagccgc                                         20
253 <210> SEQ ID NO: 11
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: antisense sequence
261 <400> SEQUENCE: 11
262 tcctgagaca ttttccagcg                                         20
265 <210> SEQ ID NO: 12
266 <211> LENGTH: 20
267 <212> TYPE: DNA
```

```
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: antisense sequence
273 <400> SEQUENCE: 12
274 ctgccggtag aacgtgggcc                                         20
277 <210> SEQ ID NO: 13
278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: antisense sequence
285 <400> SEQUENCE: 13
286 gtaagcttct gacatttcac                                         20
288 <210> SEQ ID NO: 14
289 <211> LENGTH: 20
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: antisense sequence
296 <400> SEQUENCE: 14
297 tttaggtccc tgtgaattat                                         20
300 <210> SEQ ID NO: 15
301 <211> LENGTH: 20
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: antisense sequence
308 <400> SEQUENCE: 15
309 atgttcttcc agtcaacagc                                         20
312 <210> SEQ ID NO: 16
313 <211> LENGTH: 20
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: antisense sequence
320 <400> SEQUENCE: 16
321 taaggaggtc cctgctttca                                         20
324 <210> SEQ ID NO: 17
325 <211> LENGTH: 20
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: antisense sequence
332 <400> SEQUENCE: 17
333 aaccaggtgc tcaggactcc                                         20
336 <210> SEQ ID NO: 18
337 <211> LENGTH: 20
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial Sequence
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/23/2006
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    Input Set : A:\ISPH0859USASEQ.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:172; N Pos. 429

VERIFICATION SUMMARY   DATE: 02/23/2006
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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:156 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:
L:989 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1184 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (62) SEQUENCE:
L:3006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172 after pos.:420